Amendments to the Claims

Claim 1. (currently amended) A method of determining at least one haplotype encompassing a human HLA genetic coding locus comprising:

(a) amplifying human genomic DNA, wherein the amplified genomic DNA comprises a non-coding region sequence that is in genetic linkage with an ~~the~~ HLA genetic coding locus;

(b) detecting one or more sequence variations in the non-coding region; and

(c) using the one or more non-coding region sequence variations to determine at least one haplotype encompassing the human HLA genetic coding locus.

Claim 2. (original) The method of claim 1, wherein a single haplotype is determined.

Claim 3. (original) The method of claim 1, wherein two or more haplotypes are determined.

Claim 4. (canceled)

Claim 5. (original) The method of claim 1, wherein the at least one haplotype is associated with a genetic disease.

Claim 6. (original) The method of claim 5, wherein the disease is cystic fibrosis.

Claim 7. (original) The method of claim 5, wherein the disease is phenylketonuria, muscular dystrophy or beta-thalassemia.

Claim 8. (currently amended) The method of claim 1, further comprising

(i) detecting one or more sequence variations in the coding region of the locus; and

(ii) using the one or more coding region sequence variations to determine at least one haplotype encompassing the human HLA genetic coding locus.

Claim 9. (previously presented) The method of claim 1, further comprising:

(a) analyzing DNA from a crime scene sample;

(b) analyzing DNA from a sample of a suspected perpetrator of the crime; and

(c) comparing the haplotypes present in the crime scene sample and the suspected perpetrator sample.

Claim 10. (canceled)

Claim 11. (previously presented) The method of claim 1, further comprising:

(a) analyzing DNA from an off-spring;

(b) analyzing DNA from at least one suspected parent; and

(c) comparing the haplotypes present in the offspring's DNA and in the suspected parent's DNA.

Claim 12. (original) The method of claim 1, wherein the amplified genomic DNA further comprises at least part of at least one exon.

Claim 13. (currently amended) A method for determining at least one haplotype encompassing a multi-allelic human HLA genetic coding locus comprising:

(a) amplifying human genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said HLA genetic coding locus and contains a sufficient number of non-coding region sequence nucleotides to produce an amplified DNA sequence characteristic of said at least one haplotype;

(b) analyzing the amplified DNA sequence to detect one or more sequence variations in the non-coding region; and

(c) using the one or more non-coding region sequence variations to determine at least one haplotype encompassing the multiallelic human HLA genetic coding locus.

Claim 14. (original) The method of claim 13, wherein a single haplotype is determined.

Claim 15. (original) The method of claim 13, wherein two or more haplotypes are determined.

Claim 16. (canceled)

Claim 17. (original) The method of claim 13, wherein the at least one haplotype is associated with a genetic disease.

Claim 18. (original) The method of claim 17, wherein the genetic disease is associated with variations in a regulatory or other untranslated region of the genetic locus.

Claim 19. (currently amended) A method for determining at least one haplotype encompassing a human HLA coding locus comprising:

(a) amplifying human genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said HLA coding locus;

(b) analyzing the amplified DNA sequence to detect one or more sequence variations in the non-coding region; and

(c) using the one or more non-coding region sequence variations to determine at least one haplotype encompassing the human HLA coding locus.

Claim 20. (original) The method of claim 19, wherein a single haplotype is determined.

Claim 21. (original) The method of claim 19, wherein two or more haplotypes are determined.

Claim 22. (canceled)

Claim 23. (previously presented) The method of claim 19, further comprising:

(a) analyzing DNA from a crime scene sample;

(b) analyzing DNA from a sample of a suspected perpetrator of the crime; and

(c) comparing the haplotypes present in the crime scene sample and the suspected perpetrator sample.

Claim 24. (canceled)

Claim 25. (previously presented) The method of claim 19, further comprising:

(i) analyzing DNA from an off-spring;

(ii) analyzing DNA from at least one suspected parent; and

(iii) comparing the haplotypes present in the offspring's DNA and in the suspected parent's DNA.

Claim 26. (previously presented) The method of claim 1, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

Claim 27. (previously presented) The method of claim 1, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

Claim 28. (previously presented) The method of claim 13, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

Claim 29. (previously presented) The method of claim 19, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

Claim 30. (previously presented) The method of claim 19, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

Claims 31-46. (canceled)